

ID NOS:67-811.

33. (Amended) The array of claim 32 wherein the open reading frame is differentially expressed during the cell cycle.

34. (Amended) The array of claim 32 wherein the open reading frame comprises a SAGE tag selected from the group consisting of SEQ ID NOS:67, 68, 70, 71, 72, 83, 91, and 93.

35. (Amended) The array of claim 32 which comprises at least 100 probes, wherein each probe has a sequence that is different from each other sequence.

36. (Amended) The array of claim 32 which comprises at least 500 probes, wherein each probe has a sequence that is different from each other sequence.

37. (Amended) The array of claim 32 which comprises at least 1,000 probes, wherein each probe has a sequence that is different from each other sequence.

43. (Amended) The array of claim 32 which comprises at least one probe comprising at least 14 contiguous nucleotides of each of the open reading frames identified by the SAGE tags shown in SEQ ID NOS:67-811.

44. (Amended) The array of claim 43 wherein the at least one probe of each of the open reading frames comprises a SAGE tag.

### IN THE SPECIFICATION

Please add the following paragraph to the specification on page 1, after the paragraph which contains the cross-reference to related applications and the statement regarding federally sponsored research:

--This application incorporates by reference the sequence listing contained on each of two duplicate compact discs, which are part of the application file. The sequence listing is a 15,594 KB ASCII file named "Serial No. 09-335,032

123  
1000T.  
sequence listing.txt," created on April 10, 2001.--

Delete the paragraph bridging pages 15-16 (from page 15, line 22, to page 16, line 2) and substitute the following paragraph:

B<sup>4</sup>  
A comprehensive analysis for NORF genes was performed using the SAGE data. Yeast genome intergenic regions were defined as regions outside annotated ORFs or the 500bp region downstream of annotated ORFs (yeast genome sequence and tables of annotated ORFs were obtained from SGD at the Stanford Saccharomyces genome website). Based on sequence analysis a total of 9524 putative ORFs of 25-99 amino acids were present in the intergenic regions; 510 of these ORFs contain or are adjacent to observed SAGE tags (Table 6). Of the 60,633 SAGE tags analyzed, there were 302 unique SAGE tags either within or adjacent to intergenic ORFs (100bp upstream or 500bp downstream of the ORF) (Table 6). Note that in some cases, more than one NORF contains or is adjacent to the SAGE tag. These tags matched the genome uniquely, were in the correct orientation, and were expressed at levels greater than 0.3 transcript copies per cell.

Delete the paragraph bridging pages 19-20 (from page 19, line 26, to page 20, line 8) and substitute the following paragraph:

15  
As very sparse data are available for yeast mRNA sequences and efforts to date have not been able to identify a highly conserved polyadenylation signal (Irniger and Braus, 1994; Zaret and Sherman, 1982), we used 14 bp of SAGE tags (i.e. the NlaIII site plus the adjacent 10 bp) to search the yeast genome directly (yeast genome sequence obtained from the Stanford yeast genome ftp site on August 7, 1996, SEQ ID NOS:12,204-12,219). Because only coding regions are annotated in the yeast genome, and SAGE tags can be derived from 3' untranslated regions of genes, a SAGE tag was considered to correspond to a